

REMARKS

I. RESTRICTION

Applicant hereby elects, without traverse, the invention of Group I, claims 1-5, 7-13, and 15-29, (as amended).

II. ADDITIONAL CLAIMS

Applicant respectfully requests consideration and allowance of newly added claims 31-36 which should be included as part of the invention of Group I.

Date: 3/25/02

Respectfully submitted,

By: 

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EXHIBIT A

**VERSION OF CLAIMS WITH
MARKINGS TO SHOW CHANGES MADE**

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MAR 2 9 2002

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1. (Once Amended) A method of selecting and/or identifying one or more protein affinity ligands, wherein the affinity ligands are antibodies, that bind to one or more proteins of interest, comprising the steps of:

(A) obtaining a real or theoretical mass spectrometry based characterization [peptide mass fingerprint or other mass spectrometry based characterisation or other protein characterisation] of the one or more proteins by either:

i. Subjecting the one or more proteins to a mass spectrometry based characterization [peptide mass fingerprinting or other mass spectrometry based characterisation or other protein characterisation]; or

ii. Predicting the mass spectrometry based characterization [peptide mass fingerprint or other mass spectrometry based characterisation or other protein characterisation] from known data.

(B) utilising the one or more proteins either individually or as a mixture to:

i. Generate one or more antibodies thereto by immunisation; and/or

ii. Select, using a single or multiple rounds of binding, one or more antibodies [protein affinity ligands] thereto;

(C) screening the one or more antibodies generated in step B(i) and/or the one or more antibodies [protein affinity ligands] selected in step (B)(ii) by:

i. adding the one or more proteins individually or as a mixture of proteins to the one or more antibodies [protein affinity ligands] generated in step (B)(i) or the one or more antibodies [protein affinity ligands] selected in step (B)(ii), each antibody [or protein affinity ligand] being used individually, and

ii. after removing any proteins which have not bound, eluting the at least one protein that has bound;

(D) subjecting the at least one eluted protein to a mass spectrometry based characterization [peptide mass fingerprinting and/or other mass spectrometry based characterisation and/or other protein characterisation]; and

(E) by comparing the mass spectrometry based characterization [peptide mass fingerprints or other mass spectrometry based characterisation or other protein

characterisation] obtained in steps (A) and (D) selecting and/or identifying the at least one antibody [protein affinity ligand] that binds to the one or more proteins of interest.

15. (Once amended) A method of screening an antibody [affinity ligand] to a protein characterised in that the antibody [affinity ligand] is generated or selected using an impure protein or a complex protein mixture and then identified by comparing a mass spectrometry based characterization [peptide mass fingerprint or other mass spectrometry based characterisation or other protein characterisation] obtained from the protein/proteins for which it is specific with that of a mass spectrometry based characterization [peptide mass fingerprint or other mass spectrometry based characterisation or other protein characterisation] which is theoretical for said protein/proteins or is obtained from the impure protein or complex protein mixture.

16. (Once amended) A method of selecting an antibody [or other protein affinity ligand] specific to a given peptide characterised in that the antibody [or other protein affinity ligand] is selected by comparing a mass spectrometry based characterization [peptide mass fingerprint or other mass spectrometry based characterisation or other protein characterisation] of the protein/proteins released from the antibody [or other protein affinity ligand] to which it binds with a mass spectrometry based characterization [peptide mass fingerprint or other mass spectrometry based characterisation or other protein characterisation] which is theoretical for said protein/proteins or is obtained from the known protein.

31. (New) The method of claim 1 wherein said mass spectrometry based characterization is a peptide mass fingerprint.

32. (New) The method of claim 15 wherein said mass spectrometry based characterization is a peptide mass fingerprint.

33. (New) The method of claim 16 wherein said mass spectrometry based characterization is a peptide mass fingerprint.

34. (New) A method of selecting and/or identifying at least one antibody which binds at least one protein of interest, comprising the steps of:

(A) obtaining a pre-selected mass spectrometry-based characterization of a target protein to serve as a reference standard;

(B) providing an antibody which selectively binds to said target protein;

(C) isolating and collecting said target protein through affinity binding with said antibody;

(D) analyzing said collected target protein for said pre-selected mass spectrometry-based characterization; and

(E) comparing the mass spectrometry-based characterization obtained in step (D) with the reference standard of step (A).

35. The method of selecting and/or identifying at least one antibody which binds at least one protein of interest recited in claim 34 wherein said mass spectrometry-based characterization is a peptide mass fingerprint.

36. The method of claim 35, further comprising the step of obtaining an additional mass spectrometry-based characterization in addition to said peptide mass fingerprint.